

Amendments to the Claims

This listing of claims will replace all prior versions and listings of all claims in the application.

1. (Currently amended) A method of screening for ~~generating~~ a protozymes, said method comprising:
 - a) identifying a suitable protein scaffold lacking a desirable enzyme-like activity;
 - b) inputting a protein backbone structure of said protein scaffold into a computer, wherein said backbone structure has variable residue positions ;
 - c) inserting an active site domain into said scaffold;
 - d) applying at least one protein design cycle; ~~and~~
 - e) generating a set of candidate variant proteins with putative enzyme-like activity[[]];
 - f) synthesizing a plurality of said candidate variant proteins with putative enzyme-like activity; and,
 - g) testing said candidate variant proteins with putative enzyme-like activity and selecting at least one of said candidate variant proteins with enzyme-like activity.
2. (Original) A method according to claim 1 wherein said insertion step is done at the same time as said protein design cycle.
3. (Withdrawn) A method according to claim 1 wherein said insertion step is done prior to said applying step.
4. (Withdrawn) A method according to claim 1 wherein said insertion step is done after said applying step.
5. (Original) A method according to claim 1 wherein said insertion step comprises the use of at least one high energy state rotamer.
6. (Original) A method according to claim 1 further comprising applying a second protein design cycle prior to said generating step.
7. (Original) A method according to claim 1 wherein said active site domain catalyzes a known enzymatic reaction.
8. (Withdrawn) A method according to claim 1 wherein said active site domain catalyzes an unknown enzymatic reaction.
9. (Withdrawn) A method according to claim 1 wherein said active site domain is a ligand binding domain.
10. (Original) A method according to claim 1 wherein said protein design cycle comprises a DEE computation

11. (Original) A method according to claim 1 wherein said protein design cycle includes the use of at least one scoring function.
12. (Currently amended) A method according to claim ~~[[8]]~~11 wherein said scoring function is selected from the group consisting of a van der Waals potential scoring function, a hydrogen bond potential scoring function, an atomic solvation scoring function, an electrostatic scoring function and a secondary structure propensity scoring function.
13. (Original) A method according to claim 1 further comprising synthesizing a plurality of secondary sequences to generate a library of putative protoenzymes.
14. (Original) A method according to claim 13 wherein said synthesis includes a shuffling step.
15. (Cancelled)
16. (Original) A method according to claim 1 wherein said protein design cycle comprises protein design automation.
17. (Original) A method according to claim 1 wherein said protein design cycle comprises a force field calculation.